

# SEQUENCE LISTING



E7

<110> ROULEAU, Guy A.  
JOOBER, Ridha  
BENKELFAT, Chawki

<120> POLYMORPHIC CAG REPEAT-CONTAINING GENE AND USES THEREOF

<130> 2055GG/48747TR

<140> 09/508,821

<141> 2000-05-26

<150> PCT/CA98/00884

<151> 1998-09-18

<150> 2,216,057 CA

<151> 1997-09-19

<160> 23

<170> PatentIn Ver. 2.1

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<212> DNA

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5283

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Leu Pro Leu Ser Ser Thr Met His Leu Gly Pro Val Val Ser Lys Ala  
1665 1670 1675

ctg agt acc tct tgc ctt gtt tgc tgc ctc tgc caa aac ccg gcc aac  
5571

Leu Ser Thr Ser Cys Leu Val Cys Cys Leu Cys Gln Asn Pro Ala Asn  
1680 1685 1690

ttc aag gac ctt ggg gac ctc tgt ggg ccc tac tac cct gaa cac tgc  
5619

Phe Lys Asp Leu Gly Asp Leu Cys Gly Pro Tyr Tyr Pro Glu His Cys  
1695 1700 1705 1710

ctc ccc aaa aag aag cca aaa ctc aag gag aag gtg cgg cca gaa ggc  
5667

Leu Pro Lys Lys Lys Pro Lys Leu Lys Glu Lys Val Arg Pro Glu Gly  
1715 1720 1725

acc tgt gag gag gcc tcg ctg ccg ctt gag aga aca ctc aaa ggt ccc  
5715

Thr Cys Glu Glu Ala Ser Leu Pro Leu Glu Arg Thr Leu Lys Gly Pro  
1730 1735 1740

gag tgt gca gct gcc gcc act gcc ggg aag ccc ccc agg tga cgg ccc  
5763

Glu Cys Ala Ala Ala Ala Thr Ala Gly Lys Pro Pro Arg Arg Pro  
1745 1750 1755

agc tga ccc ggc caa gca ggg ccc act gcg cac cag tgc ccg ggg cct  
5811

Ser Pro Gly Gln Ala Gly Pro Thr Ala His Gln Cys Pro Gly Pro  
1760 1765 1770

gtc ccg gag gct gca gag ctg cta ctg ctg tga tgg ccg gga gga tgg  
5859

Val Pro Glu Ala Ala Glu Leu Leu Leu Leu Trp Pro Gly Gly Trp  
1775 1780 1785 1790

ggg cga gga ggc agc ccc agc cga caa ggg tcg caa aca tga gtg cag  
5907

Gly Arg Gly Gly Ser Pro Ser Arg Gln Gly Ser Gln Thr Val Gln  
 1795 1800 1805

caa gga ggc tcc ggc aga gcc cgg cgg gga ggc cca gga gca ctg ggt  
 5955

Gln Gly Gly Ser Gly Arg Ala Arg Gly Gly Pro Gly Ala Leu Gly  
 1810 1815 1820

gca tga ggc ctg tgc cgt gtg gac cgg cgg cgt cta cct ggt ggc cgg  
 6003

Ala Gly Leu Cys Arg Val Asp Arg Arg Arg Leu Pro Gly Gly Arg  
 1825 1830 1835

gaa gct ctt tgg gct gca g  
 6022

Glu Ala Leu Trp Ala Ala  
 1840

<210> 6  
 <211> 1755  
 <212> PRT  
 <213> Homo sapiens

<400> 6  
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 Tyr Gln Gln Thr Ser Gln Glu Thr Ser Arg Leu Glu Asn Tyr Arg Gln  
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 Pro Ser Gln Ala Gly Leu Ser Cys Asp Arg Gln Arg Leu Leu Ala Lys  
 35 40 45  
 Asp Tyr Tyr Asn Pro Gln Pro Tyr Pro Ser Tyr Glu Gly Gly Ala Gly  
 50 55 60  
 Thr Pro Ser Gly Thr Ala Ala Ala Val Ala Ala Asp Lys Tyr His Arg  
 65 70 75 80  
 Gly Ser Lys Ala Leu Pro Thr Gln Gln Gly Leu Gln Gly Arg Pro Ala  
 85 90 95  
 Phe Pro Gly Tyr Gly Val Gln Asp Ser Ser Pro Tyr Pro Gly Arg Tyr  
 100 105 110  
 Ala Gly Glu Glu Ser Leu Gln Ala Trp Gly Ala Pro Gln Pro Pro Pro  
 115 120 125  
 Pro Gln Pro Gln Pro Leu Pro Ala Gly Val Ala Lys Tyr Asp Glu Asn  
 130 135 140  
 Leu Met Lys Lys Thr Ala Val Pro Pro Ser Arg Gln Tyr Ala Glu Gln  
 145 150 155 160  
 Gly Ala Gln Val Pro Phe Arg Thr His Ser Leu His Val Gln Gln Pro  
 165 170 175  
 Pro Pro Pro Gln Gln Pro Leu Ala Tyr Pro Lys Leu Gln Arg Gln Lys  
 180 185 190  
 Leu Gln Asn Asp Ile Ala Ser Pro Leu Pro Phe Pro Gln Gly Thr His  
 195 200 205  
 Phe Pro Gln His Ser Gln Ser Phe Pro Thr Ser Ser Thr Tyr Ser Ser  
 210 215 220  
 Ser Val Gln Gly Gly Gly Gln Gly Ala His Ser Tyr Lys Ser Cys Thr  
 225 230 235 240  
 Ala Pro Thr Ala Gln Pro His Asp Arg Pro Leu Thr Ala Ser Ser Ser  
 245 250 255  
 Leu Ala Pro Gly Gln Arg Val Gln Asn Leu His Ala Tyr Gln Ser Gly  
 260 265 270  
 Arg Leu Ser Tyr Asp Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln  
 275 280 285  
 Gln Gln Gln Ala Leu Gln Ser Arg His His Ala Gln Glu Thr Leu His  
 290 295 300  
 Tyr Gln Asn Leu Ala Lys Tyr Gln His Tyr Gly Gln Gln Gly Gln Gly  
 305 310 315 320  
 Tyr Cys Gln Pro Asp Ala Ala Val Arg Thr Pro Glu Gln Tyr Tyr Gln

				325					330				335				
Thr	Phe	Ser	Pro	Ser	Ser	Ser	His	Ser	Pro	Ala	Arg	Ser	Val	Gly	Arg		
			340					345					350				
Ser	Pro	Ser	Tyr	Ser	Ser	Thr	Pro	Ser	Pro	Leu	Met	Pro	Asn	Leu	Glu		
		355					360					365					
Asn	Phe	Pro	Tyr	Ser	Gln	Gln	Pro	Leu	Ser	Thr	Gly	Ala	Phe	Pro	Ala		
	370				375						380						
Gly	Ile	Thr	Asp	His	Ser	His	Phe	Met	Pro	Leu	Leu	Asn	Pro	Ser	Pro		
385				390						395					400		
Thr	Asp	Ala	Thr	Ser	Ser	Val	Asp	Thr	Gln	Ala	Gly	Asn	Cys	Lys	Pro		
				405					410					415			
Leu	Gln	Lys	Asp	Lys	Leu	Pro	Glu	Asn	Leu	Leu	Ser	Asp	Leu	Ser	Leu		
			420					425					430				
Gln	Ser	Leu	Thr	Ala	Leu	Thr	Leu	Gln	Val	Glu	Asn	Ile	Ser	Asn	Thr		
		435					440					445					
Val	Gln	Gln	Leu	Leu	Leu	Ser	Lys	Ala	Ala	Val	Pro	Gln	Lys	Lys	Gly		
	450					455					460						
Val	Lys	Asn	Leu	Val	Ser	Arg	Thr	Pro	Glu	Gln	His	Lys	Ser	Gln	His		
465					470					475					480		
Cys	Ser	Pro	Glu	Gly	Ser	Gly	Tyr	Ser	Ala	Glu	Pro	Ala	Gly	Thr	Pro		
				485					490					495			
Leu	Ser	Glu	Pro	Pro	Ser	Ser	Thr	Pro	Gln	Ser	Thr	His	Ala	Glu	Pro		
			500					505					510				
Gln	Glu	Ala	Asp	Tyr	Leu	Ser	Gly	Ser	Glu	Asp	Pro	Leu	Glu	Arg	Ser		
		515					520					525					
Phe	Leu	Tyr	Cys	Asn	Gln	Ala	Arg	Gly	Ser	Pro	Ala	Arg	Val	Asn	Ser		
	530				535						540						
Asn	Ser	Lys	Ala	Lys	Pro	Glu	Ser	Val	Ser	Thr	Cys	Ser	Val	Thr	Ser		
545					550					555					560		
Pro	Asp	Asp	Met	Ser	Thr	Lys	Ser	Asp	Asp	Ser	Phe	Gln	Ser	Leu	His		
				565					570					575			
Gly	Ser	Leu	Pro	Leu	Asp	Ser	Phe	Ser	Lys	Phe	Val	Ala	Gly	Glu	Arg		
			580					585					590				
Asp	Cys	Pro	Arg	Leu	Leu	Leu	Ser	Ala	Leu	Ala	Gln	Glu	Asp	Leu	Ala		
		595					600					605					
Ser	Glu	Ile	Leu	Gly	Leu	Gln	Glu	Ala	Ile	Gly	Glu	Lys	Ala	Asp	Lys		
	610					615						620					
Ala	Trp	Ala	Glu	Ala	Pro	Ser	Leu	Val	Lys	Asp	Ser	Ser	Lys	Pro	Pro		
625					630					635					640		
Phe	Ser	Leu	Glu	Asn	His	Ser	Ala	Cys	Leu	Asp	Ser	Val	Ala	Lys	Ser		
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Ala	Trp	Pro	Arg	Pro	Gly	Glu	Pro	Glu	Ala	Leu	Pro	Asp	Ser	Leu	Gln		
			660					665					670				
Leu	Asp	Lys	Gly	Gly	Asn	Ala	Lys	Asp	Phe	Ser	Pro	Gly	Leu	Phe	Glu		
		675					680					685					
Asp	Pro	Ser	Val	Ala	Phe	Ala	Thr	Pro	Asp	Pro	Lys	Lys	Thr	Thr	Gly		
	690					695					700						
Pro	Leu	Ser	Phe	Gly	Thr	Lys	Pro	Thr	Leu	Gly	Val	Pro	Ala	Pro	Asp		
705					710					715					720		
Pro	Thr	Thr	Ala	Ala	Phe	Asp	Cys	Phe	Pro	Asp	Thr	Thr	Ala	Ala	Ser		
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Ser	Ala	Asp	Ser	Ala	Asn	Pro	Phe	Ala	Trp	Pro	Glu	Glu	Asn	Leu	Gly		
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Asp	Ala	Cys	Pro	Arg	Trp	Gly	Leu	His	Pro	Gly	Glu	Leu	Thr	Lys	Gly		
		755					760					765					
Leu	Glu	Gln	Gly	Gly	Lys	Ala	Ser	Asp	Gly	Ile	Ser	Lys	Gly	Asp	Thr		
	770					775					780						
His	Glu	Ala	Ser	Ala	Cys	Leu	Gly	Phe	Gln	Glu	Glu	Asp	Pro	Pro	Gly		
785					790					795					800		
Glu	Lys	Val	Ala	Ser	Leu	Pro	Gly	Asp	Phe	Lys	Gln	Glu	Glu	Val	Gly		
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Gly	Val	Lys	Glu	Ala	Gly	Gly	Leu	Leu	Gln	Cys	Pro	Glu	Val	Ala			
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Lys	Ala	Asp	Arg	Trp	Leu	Glu	Asp	Ser	Arg	His	Cys	Cys	Ser	Thr	Ala		
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Asp	Phe	Gly	Asp	Leu	Pro	Leu	Leu	Pro	Pro	Thr	Ser	Arg	Lys	Glu	Asp		

850	855	860
Leu Glu Ala Glu Glu Glu Tyr Ser Ser Leu Cys Glu Leu Leu Gly Ser		
865	870	875
Pro Glu Gln Arg Pro Gly Met Gln Asp Pro Leu Ser Pro Lys Ala Pro		
	885	890
Leu Ile Cys Thr Lys Glu Glu Val Glu Glu Val Leu Asp Ser Lys Ala		
	900	905
Gly Trp Gly Ser Pro Cys His Leu Ser Gly Glu Ser Val Ile Leu Leu		
	915	920
Gly Pro Thr Val Gly Thr Glu Ser Lys Val Gln Ser Trp Phe Glu Ser		
	930	935
Ser Leu Ser His Met Lys Pro Gly Glu Glu Gly Pro Asp Gly Glu Arg		
945	950	955
Ala Pro Gly Asp Ser Thr Thr Ser Asp Ala Ser Leu Ala Gln Lys Pro		
	965	970
Asn Lys Pro Ala Val Pro Glu Ala Pro Ile Ala Lys Lys Glu Pro Val		
	980	985
Pro Arg Gly Lys Ser Leu Arg Ser Arg Arg Val His Arg Gly Leu Pro		
	995	1000
Glu Ala Glu Asp Ser Pro Cys Arg Ala Pro Val Leu Pro Lys Asp Leu		
	1010	1015
Leu Leu Pro Glu Ser Cys Thr Gly Pro Pro Gln Gly Gln Met Glu Gly		
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Ala Gly Ala Pro Gly Arg Gly Ala Ser Glu Gly Leu Pro Arg Met Cys		
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Thr Arg Ser Leu Thr Ala Leu Ser Glu Pro Arg Thr Pro Gly Pro Pro		
	1060	1065
Gly Leu Thr Thr Thr Pro Ala Pro Pro Asp Lys Leu Gly Gly Lys Gln		
	1075	1080
Arg Ala Ala Phe Lys Ser Gly Lys Arg Val Gly Lys Pro Ser Pro Lys		
	1090	1095
Ala Ala Ser Ser Pro Ser Asn Pro Ala Ala Leu Pro Val Ala Ser Asp		
1105	1110	1115
Ser Ser Pro Met Gly Ser Lys Thr Lys Glu Thr Asp Ser Pro Ser Thr		
	1125	1130
Pro Gly Lys Asp Gln Arg Ser Met Ile Leu Arg Ser Arg Thr Lys Thr		
	1140	1145
Gln Glu Ile Phe His Ser Lys Arg Arg Arg Pro Ser Glu Gly Arg Leu		
	1155	1160
Pro Asn Cys Arg Ala Thr Lys Lys Leu Leu Asp Asn Ser His Leu Pro		
	1170	1175
Ala Thr Phe Lys Val Ser Ser Ser Pro Gln Lys Glu Gly Arg Val Ser		
1185	1190	1195
Gln Arg Ala Arg Val Pro Lys Pro Gly Ala Gly Ser Lys Leu Ser Asp		
	1205	1210
Arg Pro Leu His Ala Leu Lys Arg Lys Ser Ala Phe Met Ala Pro Val		
	1220	1225
Pro Thr Lys Lys Arg Asn Leu Val Leu Arg His Gly Ser Ser Ser Ser		
	1235	1240
Ser Asn Ala Ser Ala Met Gly Glu Met Gly Arg Arg Arg Gly Leu Arg		
	1250	1255
Val Pro Pro Pro Ser Ser Arg Gly Cys Leu Leu Pro Arg Lys Pro Ser		
1265	1270	1275
Pro Pro Arg Ala Met Ala Ser Leu Pro Gln Ser Ser His Pro Arg Arg		
	1285	1290
Pro Pro Phe Leu Pro Gln Ala Arg Leu Ser Ala Ala Phe Gln Gly Ala		
	1300	1305
Met Lys Thr Lys Val Leu Pro Pro Arg Lys Gly Arg Gly Leu Lys Leu		
	1315	1320
Glu Ala Ile Val Gln Lys Ile Thr Ser Pro Ser Leu Lys Lys Phe Ala		
	1330	1335
Cys Lys Ala Pro Gly Ala Ser Pro Gly Asn Pro Leu Ser Pro Ser Leu		
1345	1350	1355
Ser Asp Lys Asp Arg Gly Leu Lys Gly Ala Gly Gly Ser Pro Val Gly		
	1365	1370
Val Glu Glu Gly Leu Val Asn Val Gly Thr Gly Gln Lys Leu Pro Thr		

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 Ser Gly Ala Asp Pro Leu Cys Arg Asn Pro Thr Asn Arg Ser Leu Lys  
 1395 1400 1405  
 Gly Lys Leu Met Asn Ser Lys Lys Leu Ser Ser Thr Asp Cys Phe Lys  
 1410 1415 1420  
 Thr Glu Ala Phe Thr Ser Pro Glu Ala Leu Gln Pro Gly Gly Thr Ala  
 1425 1430 1435 1440  
 Leu Ala Pro Lys Lys Arg Ser Arg Lys Gly Arg Ala Gly Ala His Gly  
 1445 1450 1455  
 Leu Ser Lys Gly Pro Leu Glu Lys Arg Pro Tyr Leu Gly Pro Ala Leu  
 1460 1465 1470  
 Leu Leu Thr Pro Arg Asp Arg Ala Ser Gly Thr Gln Gly Ala Ser Glu  
 1475 1480 1485  
 Asp Asn Ser Gly Gly Gly Gly Lys Lys Pro Lys Met Glu Glu Leu Gly  
 1490 1495 1500  
 Pro Ala Ser Gln Pro Pro Glu Gly Arg Pro Cys Gln Pro Gln Thr Arg  
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 Ala Gln Lys Gln Pro Gly His Thr Asn Tyr Ser Ser Tyr Ser Lys Arg  
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 Lys Arg Leu Thr Arg Gly Arg Ala Lys Asn Thr Thr Ser Ser Pro Cys  
 1540 1545 1550  
 Lys Gly Arg Ala Lys Arg Arg Arg Gln Gln Gln Val Leu Pro Leu Asp  
 1555 1560 1565  
 Pro Ala Glu Pro Glu Ile Arg Leu Lys Tyr Ile Ser Ser Cys Lys Arg  
 1570 1575 1580  
 Leu Arg Ser Asp Ser Arg Thr Pro Ala Phe Ser Pro Phe Val Arg Val  
 1585 1590 1595 1600  
 Glu Lys Arg Asp Ala Phe Thr Thr Ile Cys Thr Val Val Asn Ser Pro  
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 Gly Asp Ala Pro Lys Pro His Arg Lys Pro Ser Ser Ser Ala Ser Ser  
 1620 1625 1630  
 Ser Ser Ser Ser Ser Phe Ser Leu Asp Ala Ala Gly Ala Ser Leu  
 1635 1640 1645  
 Ala Thr Leu Pro Gly Gly Ser Ile Leu Gln Pro Arg Pro Ser Leu Pro  
 1650 1655 1660  
 Leu Ser Ser Thr Met His Leu Gly Pro Val Val Ser Lys Ala Leu Ser  
 1665 1670 1675 1680  
 Thr Ser Cys Leu Val Cys Cys Leu Cys Gln Asn Pro Ala Asn Phe Lys  
 1685 1690 1695  
 Asp Leu Gly Asp Leu Cys Gly Pro Tyr Tyr Pro Glu His Cys Leu Pro  
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 Lys Lys Lys Pro Lys Leu Lys Glu Lys Val Arg Pro Glu Gly Thr Cys  
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 Glu Glu Ala Ser Leu Pro Leu Glu Arg Thr Leu Lys Gly Pro Glu Cys  
 1730 1735 1740  
 Ala Ala Ala Ala Thr Ala Gly Lys Pro Pro Arg  
 1745 1750 1755

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 <212> PRT  
 <213> Homo sapiens

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 1 5 10 15  
 Glu Ala Ala Glu Leu Leu Leu Leu  
 20

<210> 8  
 <211> 18  
 <212> PRT  
 <213> Homo sapiens

<400> 8  
Trp Pro Gly Gly Trp Gly Arg Gly Gly Ser Pro Ser Arg Gln Gly Ser  
1 5 10 15  
Gln Thr

<210> 9  
<211> 19  
<212> PRT  
<213> Homo sapiens

<400> 9  
Val Gln Gln Gly Gly Ser Gly Arg Ala Arg Arg Gly Gly Pro Gly Ala  
1 5 10 15  
Leu Gly Ala

<210> 10  
<211> 20  
<212> PRT  
<213> Homo sapiens

<400> 10  
Gly Leu Cys Arg Val Asp Arg Arg Arg Leu Pro Gly Gly Arg Glu Ala  
1 5 10 15  
Leu Trp Ala Ala  
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<211> 22  
<212> DNA  
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<220>  
<223> Description of Artificial Sequence:  
oligonucleotide

<400> 11  
tggccttgct gcccgtagtg ct

22

<210> 12  
<211> 30  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: synthetic  
sequence = (CAR)2(CAG)n=7-12 CAA wherein n = 7

<220>  
<221> variation  
<222> (3)  
<223> R = A or G

<220>  
<221> variation  
<222> (6)  
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<400> 12  
carcargc agcagcagca gcagcagcaa

30

<210> 13  
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<212> DNA  
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<220>  
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<221> variation  
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<220>  
<221> variation  
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<400> 13  
carcarcagc agcagcagca gcagcagcag caa

33

<210> 14  
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<220>  
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sequence = (CAR)2(CAG)n=7-12 CAA wherein n = 9

<220>  
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<220>  
<221> variation  
<222> (6)  
<223> R = A or G

<400> 14  
carcarcagc agcagcagca gcagcagcag cagcaa

36

<210> 15  
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<212> DNA  
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<220>  
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sequence = (CAR)2(CAG)n=7-12 CAA wherein n = 10

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<220>  
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<222> (6)  
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<400> 15

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39

<210> 16

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic  
sequence = (CAR)2(CAG)n=7-12 CAA wherein n = 11

<220>

<221> variation

<222> (3)

<223> R = A or G

<220>

<221> variation

<222> (6)

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42

<210> 17

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic  
sequence = (CAR)2(CAG)n=7-12 CAA wherein n = 12

<220>

<221> variation

<222> (3)

<223> R = A or G

<220>

<221> variation

<222> (6)

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45

<210> 18

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic  
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39

<210> 19

<211> 30

<212> DNA

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<220>  
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<210> 20  
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<223> Description of Artificial Sequence: synthetic  
sequence = (CAG)n=9-13 CAA wherein n = 10

<400> 20  
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33

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sequence = (CAG)n=9-13 CAA wherein n = 11

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36

<210> 22  
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<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: synthetic  
sequence = (CAG)n=9-13 CAA wherein n = 12

<400> 22  
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39

<210> 23  
<211> 42  
<212> DNA  
<213> Artificial Sequence

<220>  
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sequence = (CAG)n=9-13 CAA wherein n = 13

<400> 23  
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42